

- 51 -  
- 58 -  
SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- 5 (A) NAME: Transgene SA  
(B) STREET: 11 rue de Molsheim  
(C) CITY: Strasbourg  
(E) COUNTRY: France  
(F) POSTAL CODE: 67082  
(G) TELEPHONE: (33) 03 88 27 91 00  
10 (H) TELEFAX: (33) 03 88 27 91 11  
(ii) TITLE OF INVENTION: Antitumoral composition  
based on immunogenic polypeptide with  
modified cell location  
(iii) NUMBER OF SEQUENCES: 23  
15 (iv) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Tape  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patent In Release #1.0, Version  
20 #1.25 (EPO)

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 243 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(vi) ORIGINAL SOURCE:

- 30 (A) ORGANISM: human papillomavirus  
(B) STRAIN: HPV-16  
(C) INDIVIDUAL/ISOLATE: E6 protein fused F  
protein signals

(vii) IMMEDIATE SOURCE:

- 35 (B) CLONE: E6\*TMF

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

52  
- 57 -

Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala Val Leu Leu  
1 5 10 15

Thr Leu Gln Thr Pro Thr Gly Gln Ile His Trp Gly Met His Gln Lys  
20 25 30

Arg Thr Ala Met Phe Gln Asp Pro Gln Glu Arg Pro Arg Lys Leu Pro  
35 40 45

Gln Leu Cys Thr Glu Leu Gln Thr Thr Ile His Asp Ile Ile Leu Glu  
50 55 60

Cys Val Tyr Cys Lys Gln Gln Leu Leu Arg Arg Glu Val Tyr Asp Phe  
65 70 75 80

Ala Phe Arg Asp Leu Cys Ile Val Tyr Arg Asp Gly Asn Pro Tyr Ala  
85 90 95

Val Cys Asp Lys Cys Leu Lys Phe Tyr Ser Lys Ile Ser Glu Tyr Arg  
100 105 110

His Tyr Cys Tyr Ser Leu Tyr Gly Thr Thr Leu Glu Gln Gln Tyr Asn  
115 120 125

Lys Pro Leu Cys Asp Leu Leu Ile Arg Cys Ile Asn Cys Gln Lys Pro  
130 135 140

Leu Gln Arg His Leu Asp Lys Lys Gln Arg Phe His Asn Ile Arg Gly  
145 150 155 160

Arg Trp Thr Gly Arg Cys Met Ser Cys Cys Arg Ser Ser Arg Thr Arg  
165 170 175

Arg Glu Thr Gln Leu Gly Leu Ser Ser Thr Ser Ile Val Tyr Ile Leu  
180 185 190

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Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala Leu Ile Cys  
195 200 205

Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val Gly Met Ser  
210 215 220

Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys Ser Tyr Val  
225 230 235 240

Arg Ser Leu

(2) INFORMATION FOR SEQ ID NO: 2:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- 10 (iii) HYPOTHETICAL: No
- (vi) ORIGINAL SOURCE:

REPLACEMENT SHEET (RULE 26)

- (A) ORGANISM: human papillomavirus  
 (B) STRAIN: HPV-16  
 (C) INDIVIDUAL/ISOLATE: E7 fusion signals of  
 the rabies glycoprotein

5 (vii) IMMEDIATE SOURCE:

(B) CLONE: E7\*TMR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Val Pro Gln Ala Leu Leu Phe Val Pro Leu Leu Val Phe Pro Leu  
 1 5 10 15  
 Cys Phe Gly Lys Phe Pro Ile Gly Ser Met His Gly Asp Thr Pro Thr  
 20 25 30  
 Asp Ser Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala  
 50 55 60  
 Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys  
 65 70 75 80  
 Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg  
 85 90 95  
 Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile  
 100 105 110  
 Cys Ser Gln Lys Pro Arg Ser Tyr Val Leu Leu Ser Ala Gly Ala Leu  
 115 120 125  
 Thr Ala Leu Met Leu Ile Ile Phe Leu Met Thr Cys Cys Arg Arg Val  
 130 135 140  
 Asn Arg Ser Glu Pro Thr Gln His Asn Leu Arg Gly Thr Gly Arg Glu  
 145 150 155 160  
 Val Ser Val Thr Pro Gln Ser Gly Lys Ile Ile Ser Ser Trp Glu Ser  
 165 170 175  
 His Lys Ser Gly Gly Glu Thr Arg Leu  
 180 185

10

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

20

(iii) ANTI-SENSE: Yes

REPLACEMENT SHEET (RULE 26)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: human papillomavirus
- (B) STRAIN: HPV-16
- (C) INDIVIDUAL/ISOLATE: Synthetic

5 oligonucleotide oTG5118 (E7 deleted 21  
26)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TCTGAGCTGT CATTTAATTG AGTTGTCTCT GGTTC

36

10

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: No

20

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: rabies virus
- (C) INDIVIDUAL/ISOLATE: Mutagenesis  
oligonucleotide oTG5745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

25 TGCACTCAGT AATACATAGG ATCCAATAGG GAATTTCCCA AA

42

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

35

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG6390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
GTATCTCCAT GCATGGATCC TGCAGGGTTT CTCTACGT 38

5

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

15 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG6880

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
GGATCCGCCA TGGTAGATCT TGGTTTCTGA GAACAG 36

20

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

30 (vi) ORIGINAL SOURCE:

(A) ORGANISM: rabies virus

(B) STRAIN: HPV-16

(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG5377 (E6 deleted 111  
to 115)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
TGTCCAGATG TCTTTGCAGT GGCTTTTGAC AG 32

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(B) STRAIN: Synthetic oligonucleotide  
oTG10829

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

15 GCGCGCTCTA GAATTATGGG TCTCAAGGTG AACG 34

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

(B) STRAIN: Synthetic oligonucleotide  
oTG10830

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

30 CAGTTCTCTT TTGGTGCATG CCCCAATGGA TTTGA 35

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

5 (B) STRAIN: Synthetic oligonucleotide  
oTG10835

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

ATGCTAGTGC TCGATAAACC CAGCTGGGTT TCTCTACG 38

10 (2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

20 (B) STRAIN: Synthetic oligonucleotide  
oTG10836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCAAATCCAT TGGGGCATGC ACCAAAAGAG AACTG 35

25 (2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

35 (C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG10833

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG10834

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GCGGGCATGC GGTACCTCAG AGCGACCTTA CATAGG

36

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- ~~(C) STRANDEDNESS: single~~
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25 (iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: vaccinia virus

(B) STRAIN: modified Ankara

30 (C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG7637 (PCR III region)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGGGGGGAAT TCAGTAAACT TGACTAAATC TT

32

35 (2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs



- 59 -  
- 64 -

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 5 (iii) HYPOTHETICAL: No  
 (iii) ANTI-SENSE: Yes  
 (vi) ORIGINAL SOURCE:  
 (A) ORGANISM: vaccinia virus  
 (B) STRAIN: modified Ankara  
 10 (C) INDIVIDUAL/ISOLATE: Synthetic  
 oligonucleotide oTG7638 (PCR III region)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
 GGGGGGGGAT CCGAGCTCAC CAGCCACCGA AAGAGCAAT 39

15 (2) INFORMATION FOR SEQ ID NO: 16:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 20 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (iii) HYPOTHETICAL: No  
 (iii) ANTI-SENSE: No  
 (vi) ORIGINAL SOURCE:  
 25 (A) ORGANISM: vaccinia virus  
 (B) STRAIN: modified Ankara  
 (C) INDIVIDUAL/ISOLATE: Synthetic  
 oligonucleotide oTG7635 (PCR III region)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
 30 GGGGGGGGAT CCGGAAAGTT TTATAGGTAG TT 32

(2) INFORMATION FOR SEQ ID NO: 17:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

- 5 (A) ORGANISM: vaccinia virus  
(B) STRAIN: modified Ankara  
(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG7636 (PCR III region)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

10 GGGGGGGAAT TCTTTGTATT TACGTGAACG 30

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

20 (iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

- (B) STRAIN: Synthetic oligonucleotide  
oTG10502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

25 AGCTTTTAT TCTATACTTA AAAAATGAAA ATAAACTCGA GTTGTCAAAG  
CATCATCTCA AACTGACTT GAGGTAC 77

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35 (iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

(B) STRAIN: Synthetic oligonucleotide  
oTG10503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
CTCAAGTCAG TGTGAGATG ATGCTTTGAC AACTCGAGTT TATTTTCATT  
5 TTTTAAGTAT AGAATAAAA 69

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs  
10 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

15 (iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG5925

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
20 TCAGATCTGT CGAGGGATCT GCAGCTTCTT CTAGAGGTA 39

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

30 (iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL/ISOLATE: Synthetic  
oligonucleotide oTG5924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
35 AGTGAATTGC TGCAGGTACC CGGATCCGCA TCGACTATCG ACAT 44

(2) INFORMATION FOR SEQ ID NO: 22:

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

5 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

10 (iii) ANTI-SENSE: No

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapiens

(B) STRAIN: Daudi cell line

15 (C) INDIVIDUAL/ISOLATE: PCR primer oTG6353  
(cloning B7.1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TCAGCCCCTG AATTCTGCGG ACACTGTTT ACAGG 35

(2) INFORMATION FOR SEQ ID NO: 23:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: - nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: No

(iii) ANTI-SENSE: Yes

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapiens

30 (B) STRAIN: Daudi cell line

(C) INDIVIDUAL/ISOLATE: PCR primer oTG6352  
(cloning B7.1)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TTGACCCTAA AGATCTGAAG CCATGGGCCA CAC 33